AMENDMENTS TO THE CLAIMS

1. **(Previously presented)** A recombinant nucleotide sequence which codes upon expression for at least a part of a bifunctional hybrid active-site serine β-lactamase protein, wherein the β-lactamase protein is bearing at least one heterologous sequence, wherein the β-lactamase protein is bearing the heterologous sequence in a region located between two neighboring alpha helices of the β-lactamase sequence, wherein the region is forming a juncture between the alpha helices of active-site serine β-lactamases, wherein said alpha helices correspond to the last two alpha helices before the alpha/beta domain, and wherein the hybrid protein is having two functions, the first function is associated with the β-lactamase portion and the second function is associated with the heterologous sequence having a biological function which is different from the first function.

2. **(Canceled)**

3. **(Canceled)**

4. **(Currently amended)** The recombinant nucleotide sequence according to Claim 1, wherein the β-lactamase protein is bearing at least one heterologous sequence in a region located between two neighboring alpha helices of the β-lactamase sequence, wherein the region is selected from the group consisting of:

a) the region forming a juncture between alpha helix 8 and alpha helix 9 of TEM-1 β-lactamase; and

b) the region forming a juncture between the alpha helices which are homologous to alpha helix 8 and alpha helix 9 of TEM-1 β-lactamase.

5. **(Currently amended)** The recombinant nucleotide sequence according to Claim 1, wherein the β-lactamase moiety is selected from the group consisting of:

a) class A β-lactamase,

b) class C β-lactamase,

c) class D β-lactamase, and

d) a recombinant sequence of one or more of a) to c).

6. **(Currently amended)** The recombinant nucleotide sequence according to Claim 1, wherein the β-lactamase moiety is derived from class A β-lactamase, wherein β-lactamase class A protein is bearing the heterologous sequence in the region forming a juncture between alpha helix 8 and alpha helix 9.

7. **(Currently amended)** The recombinant nucleotide sequence according to claim 6, wherein the region forming a juncture between alpha helix 8 and alpha helix 9 is selected from the group consisting of:

a) the amino acid sequence Thr195 to Leu199 of the TEM-1 β-lactamase; and

b) the amino acid sequence corresponding to the amino acid sequence Thr195 to Leu199 in TEM-1 β-lactamase.

8. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the β-lactamase moiety is derived from class C β-lactamase, wherein β-lactamase class C protein is bearing the heterologous sequence in the region forming a juncture between alpha helices, which correspond to alpha helix 8 and alpha helix 9 in TEM-1 β-lactamase.

9. **(Currently amended)** The recombinant nucleotide sequence according to claim 8, wherein the region forming a juncture is selected from the group consisting of:

a) the amino acid sequence K239 to E245 of the AmpC β-lactamase; and

b) the amino acid sequence corresponding to the amino acid sequence K239 to E245 of the AmpC β-lactamase.

10. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the β-lactamase moiety is derived from class D β-lactamase, wherein β-lactamase class D protein is bearing the heterologous sequence in the region forming a juncture between alpha helices, which correspond to alpha helix 8 and alpha helix 9 in TEM-1 β-lactamase.

11. **(Currently amended)** The recombinant nucleotide sequence according to claim 10, wherein the region forming a juncture is selected from the group consisting of:

a) the amino acid sequence N510 to F514 of the BlaR-CTD β-lactamase; and

b) the amino acid sequence corresponding to the amino acid sequence N510 to F514 of the BlaR-CTD β-lactamase.

12. **(Currently amended)** A recombinant nucleotide sequence which codes upon expression for at least a part of a bifunctional hybrid β-lactamase class A protein, wherein the β-lactamase class A protein is bearing at least one heterologous sequence in a region located between two neighboring alpha helices of the β-lactamase sequence, wherein the region is selected from consisting of:

a) the region forming a juncture between alpha helix 8 and alpha helix 9 of the TEM-1 β-lactamase; and

b) the region forming a juncture between the alpha helices of homologous β-lactamases class A, said alpha helices corresponding to the alpha helix 8 and alpha helix 9 of the TEM-1 β-lactamase, ~~and~~

wherein the hybrid protein has a first function and a second function ~~is having two functions~~, wherein the first function is associated with the β-lactamase portion and is selected from the group consisting of:

c) hydrolyzing β-lactams (β-lactamase activity); and

d) binding covalently and in a stable manner to substances selected from the group β-lactams, derivatives of β-lactams, inhibitors of β-lactams;

and wherein the second function is associated with the heterologous sequence having a biological function which is different from the first function.

13. **(Canceled)**

14. **(Canceled)**

15. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the three-dimensional structure of the β-lactamase portion of the hybrid β-lactamase is homologous to the three-dimensional structure of the TEM-1 β-lactamase.

16. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence has a length of 11 or more amino acid residues.

17. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence has a length of 18 or more amino acid residues.

18. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence has a length of 25 or more amino acid residues.

19. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence has a length of 50 or more amino acid residues.

20. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence has a length of 100 or more amino acid residues.

21. **(Currently amended)** The recombinant nucleotide sequence according to Claim 1, wherein the nucleotide sequence coding for the β-lactamase sequence is selected from the group consisting of:

a) nucleotide sequence coding for the β-lactamase TEM-1 (SEQ ID NO: 1)

b) nucleotide sequence coding for the β-lactamase BlaP (SEQ I D NO: 2);

c) nucleotide sequence coding for the β-lactamase BlaL (SEQ ID NO: 3);

d) nucleotide sequence coding for the β-lactamase AmpC (SEQ ID NO: 39);

e) nucleotide sequence coding for the β-lactamase BlaR-CTD (SEQ ID NO: 41);

f) a recombinant sequence of one or more of a) to e); and

g) nucleotide sequences which hybridise under stringent conditions to the nucleotide sequences of any one of a) to f) or fragments thereof.

22. **(Currently amended)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence is related to a function selected from the group consisting of: being an epitope, being a specific binding partner for antibodies, being specifically recognized and bound by antibodies, having a binding affinity to earth alkali and metal ions, having enzymatic activity, being a toxin (STa heat-stable enterotoxin of *E. coli*), bearing a glycosylation site, bearing a glycosylated peptide, being a specific binding partner for any polypeptide or any ligand, and having a binding affinity to dsDNA and ssDNA or RNA (having a binding affinity to nucleotide and polynucleotide).

23. **(Currently amended)** The recombinant nucleotide sequence according to Claim 1, wherein the heterologous sequence is selected from the group consisting of: STa (heat stable enterotoxin of *Escherichia coli*, SEQ ID NO: 21), protein A of *Staphylococcus aureus*, (SEQ ID NO: 23 and 25), protein G of *Streptococcus pyogenes*, (SEQ ID NO: 27 and 29), a linear antigenic determinant of the hemagglutinin of the Influenza virus (SEQ ID NO: 31), a fragment of human phospholipase-type 11 (hPLA2) (SEQ ID NO: 33), LPS binding amino acid sequence (SEQ ID NO: 35), and nucleotide sequences which ~~hybridise~~ hybridize under stringent conditions to said nucleotide sequences or fragments thereof.

24. **(Canceled)**

25. **(Withdrawn)** A recombinant polypeptide comprising at least a part of a bifunctional hybrid active-site serine β-lactamase protein, wherein the β-lactamase protein is bearing at least one heterologous sequence, wherein the β-lactamase protein is bearing at least one heterologous sequence in a region located between two neighboring alpha helices of the β-lactamase sequence, wherein the region is forming a juncture between the alpha helices of active-site serine β-lactamase, wherein said alpha helices correspond to the last two alpha helices before the alpha/beta domain, and wherein the hybrid protein is having two functions, the first function

is associated with the β-lactamase portion and the second function is associated with the heterologous sequence having a biological function which is different from the first function.

26.-53. **(Canceled)**